



#6

## SEQUENCE LISTING

&lt;110&gt; MURRAY, RICHARD

<120> Novel Methods of Diagnosis of Angiogenesis,  
Compositons, and Methods of Screening for Angiogenesis  
Modulators

&lt;130&gt; A-68110-1/DJB/RMS/DCF

&lt;140&gt; US 09/637,977

&lt;141&gt; 2000-08-11

&lt;150&gt; US 60/148,425

&lt;151&gt; 1999-08-11

&lt;160&gt; 22

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1237

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1

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 Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val  
 50 55 60  
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<212> DNA

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 <212> PRT  
 <213> Homo sapiens

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 35 40 45

Pro Ala Val Leu Ser Gly Pro Pro Gly Ser Phe Phe Gly Phe Ser Val  
 50 55 60

Glu Phe Tyr Arg Pro Gly Thr Asp Gly Val Ser Val Leu Val Gly Ala  
 65 70 75 80

Pro Lys Ala Asn Thr Ser Gln Pro Gly Val Leu Gln Gly Gly Ala Val  
 85 90 95

Tyr Leu Cys Pro Trp Gly Ala Ser Pro Thr Gln Cys Thr Pro Ile Glu  
 100 105 110

Phe Asp Ser Lys Gly Ser Arg Leu Leu Glu Ser Ser Leu Ser Ser Ser  
 115 120 125

Glu Gly Glu Glu Pro Val Glu Tyr Lys Ser Leu Gln Trp Phe Gly Ala  
 130 135 140

Thr Val Arg Ala His Gly Ser Ser Ile Leu Ala Cys Ala Pro Leu Tyr  
 145 150 155 160

Ser Trp Arg Thr Glu Lys Glu Pro Leu Ser Asp Pro Val Gly Thr Cys  
 165 170 175

Tyr Leu Ser Thr Asp Asn Phe Thr Arg Ile Leu Glu Tyr Ala Pro Cys  
 180 185 190

Arg Ser Asp Phe Ser Trp Ala Ala Gly Gln Gly Tyr Cys Gln Gly Gly  
 195 200 205

Phe Ser Ala Glu Phe Thr Lys Thr Gly Arg Val Val Leu Gly Gly Pro  
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 Gly Ser Tyr Phe Trp Gln Gly Gln Ile Leu Ser Ala Thr Gln Glu Gln  
 225 230 235 240  
 Ile Ala Glu Ser Tyr Tyr Pro Glu Tyr Leu Ile Asn Leu Val Gln Gly  
 245 250 255  
 Gln Leu Gln Thr Arg Gln Ala Ser Ser Ile Tyr Asp Asp Ser Tyr Leu  
 260 265 270  
 Gly Tyr Ser Val Ala Val Gly Glu Phe Ser Gly Asp Asp Thr Glu Asp  
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 Phe Val Ala Gly Val Pro Lys Gly Asn Leu Thr Tyr Gly Tyr Val Thr  
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 Gln Met Ala Ser Tyr Phe Gly Tyr Ala Val Ala Ala Thr Asp Val Asn  
 325 330 335  
 Gly Asp Gly Leu Asp Asp Leu Leu Val Gly Ala Pro Leu Leu Met Asp  
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 Arg Thr Pro Asp Gly Arg Pro Gln Glu Val Gly Arg Val Tyr Val Tyr  
 355 360 365  
 Leu Gln His Pro Ala Gly Ile Glu Pro Thr Pro Thr Leu Thr Leu Thr  
 370 375 380  
 Gly His Asp Glu Phe Gly Arg Phe Gly Ser Ser Leu Thr Pro Leu Gly  
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 Gly Gly Glu Thr Gln Gln Gly Val Val Phe Val Phe Pro Gly Gly Pro  
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 Ala Ser His Thr Pro Asp Phe Phe Gly Ser Ala Leu Arg Gly Gly Arg  
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 Glu Leu Gln Leu Asp Trp Gln Lys Gln Lys Gly Gly Val Arg Arg Ala  
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 Asn Glu Ser Glu Phe Arg Asp Lys Leu Ser Pro Ile His Ile Ala Leu  
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 Pro Ala Leu His Tyr Gln Ser Lys Ser Arg Ile Glu Asp Lys Ala Gln  
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 660 665 670  
 Ala Leu Asn Leu Thr Phe His Ala Gln Asn Val Gly Glu Gly Gly Ala  
 675 680 685  
 Tyr Glu Ala Glu Leu Arg Val Thr Ala Pro Pro Glu Ala Glu Tyr Ser  
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755 760 765  
Ser Lys Asn Leu Asn Asn Ser Gln Ser Asp Val Val Ser Phe Arg Leu  
770 775 780  
Ser Val Glu Ala Gln Ala Gln Val Thr Leu Asn Gly Val Ser Lys Pro  
785 790 795 800  
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805 810 815  
Gln Lys Glu Glu Asp Leu Gly Pro Ala Val His His Val Tyr Glu Leu  
820 825 830  
Ile Asn Gln Gly Pro Ser Ser Ile Ser Gln Gly Val Leu Glu Leu Ser  
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Cys Pro Gln Ala Leu Glu Gly Gln Gln Leu Leu Tyr Val Thr Arg Val  
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Thr Gly Leu Asn Cys Thr Thr Asn His Pro Ile Asn Pro Lys Gly Leu  
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Glu Leu Asp Pro Glu Gly Ser Leu His His Gln Gln Lys Arg Glu Ala  
885 890 895  
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900 905 910  
Glu Ala Glu Cys Phe Arg Leu Arg Cys Glu Leu Gly Pro Leu His Gln  
915 920 925  
Gln Glu Ser Gln Ser Leu Gln Leu His Phe Arg Val Trp Ala Lys Thr  
930 935 940  
Phe Leu Gln Arg Glu His Gln Pro Phe Ser Leu Gln Cys Glu Ala Val  
945 950 955 960  
Tyr Lys Ala Leu Lys Met Pro Tyr Arg Ile Leu Pro Arg Gln Leu Pro  
965 970 975

Gln Lys Glu Arg Gln Val Ala Thr Ala Val Gln Trp Thr Lys Ala Glu  
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Gly Ser Tyr Gly Val Pro Leu Trp Ile Ile Ile Leu Ala Ile Leu Phe  
 995 1000 1005

Gly Leu Leu Leu Leu Gly Leu Leu Ile Tyr Ile Leu Tyr Lys Leu Gly  
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Leu Lys Pro Pro Ala Thr Ser Asp Ala  
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<211> 1713

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (1613)

<223> "n" at position 1613 can be any base.

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 atttgcagca gtaacagcac aggtgtttta gaggcagcta ataattcact tgttgttact 180  
 acaacaaaac catctataac aacaccaaac acagaatcat tacagaaaaa tgttgtcaca 240  
 ccaacaactg gaacaactcc taaaggaaca atcaccaatg aattacttaa aatgtctctg 300  
 atgtcaacag ctactttttt aacaagtaaa gatgaaggat tgaaagccac aaccactgat 360  
 gtcaggaaga atgactccat catttcaaac gtaacagtaa caagtgttac acttcccaat 420  
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 acctcaatac cagttacaat tccagaaaac acctcacagt ctcaagtaat agrcactgag 600  
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<212> PRT

<213> Homo sapiens

<220>

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<222> (172)

<223> "Xaa" at position 172 can be any amino acid.

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Val Thr Thr Thr Lys Pro Ser Ile Thr Thr Pro Asn Thr Glu Ser Leu  
35 40 45

Gln Lys Asn Val Val Thr Pro Thr Thr Gly Thr Thr Pro Lys Gly Thr  
50 55 60

Ile Thr Asn Glu Leu Leu Lys Met Ser Leu Met Ser Thr Ala Thr Phe  
65 70 75 80

Leu Thr Ser Lys Asp Glu Gly Leu Lys Ala Thr Thr Thr Asp Val Arg  
85 90 95

Lys Asn Asp Ser Ile Ile Ser Asn Val Thr Val Thr Ser Val Thr Leu  
100 105 110

Pro Asn Ala Val Ser Thr Leu Gln Ser Ser Lys Pro Lys Thr Glu Thr  
115 120 125

Gln Ser Ser Ile Lys Thr Thr Glu Ile Pro Gly Ser Val Leu Gln Pro  
130 135 140

Asp Ala Ser Pro Ser Lys Thr Gly Thr Leu Thr Ser Ile Pro Val Thr  
 145 150 155 160

Ile Pro Glu Asn Thr Ser Gln Ser Gln Val Ile Xaa Thr Glu Gly Gly  
 165 170 175

Lys Asn Ala Ser Thr Ser Ala Thr Ser Arg Ser Tyr Ser Ser Ile Ile  
 180 185 190

Leu Pro Val Val Ile Ala Leu Ile Val Ile Thr Leu Ser Val Phe Val  
 195 200 205

Leu Val Gly Leu Tyr Arg Met Cys Trp Lys Ala Asp Pro Gly Thr Pro  
 210 215 220

Glu Asn Gly Asn Asp Gln Pro Gln Ser Asp Lys Glu Ser Val Lys Leu  
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 gcatttggat ttttctactt cttcagtgga tcacacagt ttgagtttga ccccaatgcc 1380  
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<210> 22

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (3)

<223> The xaa at position 3 represents any amino acid.

<220>

<223> Description of Artificial Sequence: cytokine  
 receptor extracellular motif found in many species

<400> 22

Trp Ser Xaa Trp Ser

1

5



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PATENT APPLICATION

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TIME: 17:26:36

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VERIFICATION SUMMARY REPORT  
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#### GENERAL INFORMATION SECTION

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6, Compositions, and Methods of Screening for Angiogenesis  
7, Modulators  
9,<130> A-68110-1/DJB/RMS/DCF  
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W--> 890 Trp Ser Xaa Trp Ser

#### STATISTICS SUMMARY

Application Serial Number: US 09/637,977A  
Alpha or Numeric: Numeric  
Application Class:  
Application File Date: 2000-08-11  
Art Unit:  
Software Application: PatentIn  
Total Number of Sequences: 22  
Number of Errors: 0  
Number of Warnings: 3  
Number of Corrections: 0